

1 31
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151 Cadherin
|xx EC motif xx|
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661

CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721

ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781

GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

841

GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901

AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961

ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021

CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn

1081

TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141

AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201

GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261

TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321

GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

691

751

811

871

931

991

1051

1111

1171

1231

1291

1351

1381

AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441

CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501

GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561

GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621

AAAAAAAAAAAAAAAAAAAAAAAAAAAA transmembrane domain AAAAAAA
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

AAAAAAAAAAAAAAAAAAAAAAAAAAAA|

TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1741

AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801

TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861

CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921

GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981

ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041

TTTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

|xxxxx ITAM xxxx|

2071

2101

GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2131

2161

GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2191

2221

GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2251

2281

TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2311

2341

CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2371

2401

GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2431

2461

AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

2491

|xxxxxxxxxxxxxxxxxxxxxxxxxxxx

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|

2611

AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641

2671

GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701

2731

|xxxxxxxxxxxx

AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val

GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
asp STP

TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661

3721

CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

3751

3781

AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

3811

3841

CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3871

3901

TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3931

3961

GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

3991

4021

AAC TCG

.5 kb —

BRAIN
HEART
SKEL. MUSCLE
COLON
THYMUS
SPLEEN
KIDNEY
LIVER
SM. INTESTIN
PLACENTA
LUNG
PBL

Jurkat
MV4-11
THP
HL60
9D10
CH27
3A9
293

~ 7.5 kb —



B

HC2A
KIAA ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat
HC4
HC1
HC3
HC5

HC2A
KIAA FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat
HC4
HC1
HC3
HC5

HC2A
KIAA -----VLHHHQNPFEFYDEIK
rat KSAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPFEFYDEIK
HC4
HC1
HC3
HC5

HC2A
KIAA IELPTQLHEKHHLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat IELPTQLHEKHHLLLTFFHVSCDNSSKSGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC4
HC1
HC3
HC5

HC2A
KIAA PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
HC4
HC1
HC3 -----GPGPARSTVSISLISNSARV
HC5

HC2A
KIAA OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
HC4 -----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1 -----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3 NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5

HC2A I I H V V A Q C H E L G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E L G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G --- S V R --- E
 HC5 -----

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L I H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S --- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S --- M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V L V S L R L D F L
 HC5 -----

HC2A F V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 KIAA F V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S D E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D P L T P S E S --- T Q E L H A S D M P E Y S V T N E F
 HC3 F I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A M F E L S --- V P F
 HC5 ----- M N A L T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V F L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V F L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K O A Q I A S
 HC3 F Q Q H Y L A G L V L T E L A V I L L P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G L L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V F D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V F D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L L E N I Q R L A G F D T L Y S C A A M P N S A S R D E F P C G --- F T S P --- A N --- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T

HC2A KDLLGAISCSPYTTSTPNINSVRNADSRGSLISTDSGNSLPERSEKSNSLDKHQSS
 KIAA KDLLGAISCSPYTTSTPNINSVRNADSRGSLISTDSGNSLPERSEKSNSLDKHQSS
 rat -----
 HC4 TDKDTAYGSFQNG-----HGKREDSRGS LIP-EGATGFPDQGN TGEN-----TRQS
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFFTISEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFFTISEVCL
 rat -----
 HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISED TLLTYWN-KVSPQELINILILEVCL
 HC1 ALIGSTLRFDRLDQAE TRSLLMCF LHMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
 HC3 -----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLYL CV
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFOYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
 KIAA HQFOYMGKRYIAR-----TGMM
 rat -----
 HC4 FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALRNRS GVM
 HC1 QNFRYL GKRNII RKIAAAF--KFVQSTQNNGLTKGSNPSCQTSGLLAQWMHSTSRHEGHK
 HC3 SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILG SIGARQEMV
 HC5 LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat -----
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
 HC1 QHRSQTLPIIRGK---NALS NPKL---LQMLDNTMTS NSNEIDIVHHVDTEANIATEGC
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A LTALDTLSLFTLAFKNQLLADHGHNP LMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
 KIAA LTALDTLSLFTLAFKNQLLADHGHNP LMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
 rat -----
 HC4 LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
 HC1 LTILDVSLFTQTHQRQLQCCDCQNSLMKRGFDTYMLFFQV NQSATALKHVFASLRLFVC
 HC3 LIILD TLEIVVQTVS--VTES--KESILGGV LKVLHSMACNQSAVYLQHC FATQRALVS
 HC5 LIILDMQENIIQASS--ALDC--KDSL LGGVLRLV LNSLNC DQSTTYLTHCFATLRALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 rat -----
 HC4 KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 HC1 KFPFAFFKGRVNMCAAF CYEVLKCC TSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
 HC3 KFPFAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
 HC5 KFPPELLFEEETEQCADLCRLRLRHCCSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
 KFGDLLFEEVEQCFDLCHQV LHHCCSSMDVTRSQACATLYLLMRFSFGATS--NFARVK

HC2A LQVIIISVSQLIADVVVGIGGETRFQQSLSIINN CANS DRLIKHTSFSSDVKDLTKRIRTVLM
 KIAA LQVIIISVSQLIADVVVGIGGETRFQQSLSIINN CANS DRLIKHTSFSSDVKDLTKRIRTVLM
 rat -----
 HC4 LQVIIISLSQLIADVVVGIGGETRFQQSLSIINN CANS DRLIKHTSFSSDVKDLTKRIRTVLM
 HC1 LQIIIAVSQLIADVALSGGSRFQESLFIINN FANS DRPMLARAFPAEVKDLTKRIRTVLM
 HC5 LQIIKAYSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLM

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGL	LSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGL	LSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGL	LSEAAMCYVHV
HC4	ATAQMKEHEKDPPEMLIDLQYSLAKSYASTPELRKTWLD	SMAKIHVKNGL	FSEAAMCYVHV
HC1	ATAQMKEHEKDPPEMLVDLQYSLANSYASTPELRRTWLE	SMAKIHARNGD	LSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSDDLRLTWL	QNMAGKHSERSN	HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASDDLRLTWL	QNMAEKHTKKKQ	YTEAMCLVHA

	domain	SH3	
HC2A	TALVAEYILTRKGV-----		FRQGCTAFRVITPN
KIAA	TALVAEYILTRKEA-----	VQWEPPLLP	SHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYILTRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEYILHRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYILKRKGWVKEIK	TASLLSE	THPCDSNSLLTTPSGGSMFSGMGPFLSITPN
HC3	AALVAEYILSMLED-----		RKYLPGVCVTFQNISSN
HC5	AALVAEYILSMLED-----		HSYLPVGSVSFQNISSN

ITAM

HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAER	YELIADIYKLI	IPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAER	YELIADIYKLI	IPI
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAER	LRAGLLTSINSSSP	
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAER	YEI	ISEISKLGPI
HC1	IKEEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSE	YEL	IADVNKPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVL	IPI		
HC5	VLEESVVSSEDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEV	YKLV	IPI	

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRD	FERLAHL	YDTI	HRAYS
rat	SMKSGGTLETTHLYDTI	HRAYS	SKVTEVMHSGRRLLGTY	FRVAFFGQAAQYQFTDSETDVE
HC4	YENRPEFENLTQVYRTI	HGAYTKI	LEVMTTKRLLG-----	TFFRVAFYGGQ
HC1	FEKQRFKFLSDLYDYD	HRSYLKVAE	VNSEKRLFG-----	HYFRVAFYGGQ
HC3	HEANF	DAKFLSTIHGKLQ	EAFSKI	VHQSTGWERMFG-----
HC5	LEAHPEFRFLTLTHSKLQ	RAFDSIVN	KDHH--KRMFG-----	TYFRVGFFG--

	ITAM	ITAM
HC2A	-FFEDEDGHE	YIYKEPKLTP
KIAA	GFFEDEDGHE	YIYKEPKLTP
rat	GFFEDEDGHE	YIYKEPKLTP
HC4	SFFEEEDGHE	YIYKEPKLTP
HC1	GFFEEEGGHE	YIYKEPKLTP
HC3	TKFGDLDEQE	FVYKEPAITKLAE
HC5	SKFGDLDEQE	FVYKEPAITKLPE

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
HC4	HIQVTVYVKPYFDDKELTERKTEFERHNINSRFVFEAPYTLGKKGQGCIEEQCKRRTILT
HC1	YIQVTVYVTPFFEEKEIEDRKTD

Coiled-Coil 1

HC2A	IHCFFPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQ	SSV
KIAA	IHCFFPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQ	SSV
rat	IHCFFPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELHQLC	SSAEVDMIKLQLKLQ	SSV
HC4	SNSFFPYVKKRIP	INCEQQINLKE	IDGATDEIKDKTAE	LQKLCSSSTDVDM	IQQLKLQ
HC1	SHLFFPYVKKRIQ	VISQSSTELN	IEVAIDEMSRKVSELNQL	CTMEEVDMISLQLKLQ	SSV
HC3	SHAFPIKTRPVNV	THKEEII	LTBIEVAIDEMQKKTQ	ELAFATHQDPADPKMLQ	MLQ
HC5	MHAFPIKTRISVI	QKEEFVLT	BIEVAIDEMKKKT	LQLAVAINQEP	PPDAKMLQMLQ

Coiled-Coil 2

HC2A	SVQVNAGPLAYARA	FLDDTNTKRYPD	KNVKLLKEVFRQFVEAC	QQLAVNERLIKEDQ	LE
KIAA	SVQVNAGPLAYARA	FLDDTNTKRYPD	KNVKLLKEVFRQFVEAC	QQLAVNERLIKEDQ	LE
rat	SVQVNAGPLAYARA	FLDDTNTKRYPD	KNVKLLKEVFRQFVEAC	QQLAVNERLIKEDQ	LE
HC4	SVQVNAGPLAYARA	FLNDSQASKYP	PKKVSELKDMFRKFI	QACSI	LELNERLIKEDQ
HC1	SVKVNAGPMAYARA	FLNETNAKKYP	PDNQVKLLKEIFRQ	FADACQQLDVNERLIKEDQ	LE
HC3	GTTVNQGP	LEVAQVFLSEI	PSDPKLFRRH	HNKLRLCFKDF	TKRCEDALRKNKSLIGPVQKE
HC5	GATVNQGP	LEVAQVFLAEI	PADPKLYRHH	HNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE

Coiled-Coil 2

HC2A	YQEEMKANYREMA	KELSEIMHE	QICPLEEKTS-VLP	NSLHIFNAISG	TPTSTMVHG	MSS
KIAA	YQEEMKANYREMA	KELSEIMHE	QLG-----			
rat	YQEEMKANYREIR	KELSDIIVE	RICPGEDK	RATKFP	PAHLQRHQ	RDNTNKHSGSRVDQFILS
HC4	YHEGLKSNFRDM	VKELSDI	IHEQILQED	TMHSPWMS	NTHLVFCAI	SGTSSDRGYGSPRYA
HC1	YQEELRSHYK	DMLSELSTVM	NEQITGRD	DLSK---	RGVDQTCT	RVISKATPALPTVSISS
HC3	YQRELG----	KLSS-----	---	PZ-----		
HC5	YQELKKNYNKL	KENLRPMIE	RKIPELYKPI	FRVESQKRDS	FHRSSF	FRKCETQLSQSSZ-

PBM

HC2A	SSVVZ-----
KIAA	-----
rat	CVTLPH
HC4	EVZ-----
HC1	SAEVZ-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

	A	B
CLASP-1	YRVAFYGO:::GFFEEEEGKEYIYKEP	
KIAA1058	FRVAFFGQAACYQFTDSETDVEGFFEDDGKEYIYKEP	
CLASP-2		FEDEDGKEYIYKEP
CLASP-6	FRVAFFGO:::GFFEDDGKEYIYKEP	
CLASP-4	FRVAFYGO:::SFFEEEEGKEYIYKEP	
DOCK180	FAVGYYGO:::GFPTFLRGKVFIYRGKEYERRSD	
DOCK2	FAVGYYGO:::GFPSFLRNKVFIYRGKEYERRSD	
DOCK3	FRVGIFYGR:::KFPFFLRNKEYVCRGH	
KIAA0716	FRVGIFYGK:::KFPFFLRNKEFVCRGH	
CLASP-3	FRVGIFYGT:::KFGDLDEQEFVYKEP	
CONSENSUS	F V FYG YF	KEY K Q F R

	C
TRG	PKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFAYIQVTHVTPFFDEKE
CLASP-1	PKLTGLSEISQRLCLKLYADKFGADNVKIIQDSNKNVNPKDLDPKYAYIQVTYVTPFFEEKE
CLASP-2	PKLTPLSEISQRLCLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKE
CLASP-4	PKLTGLSEISLRLVKLYGEKFGTENVKIIQSDSKVNAKELDPKYAYIQVTYVKPYFDKE
CLASP-3	PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEPYFDIYE
KIAA0716	HDYERLEAFQQRMLNEFPHTAIA-----MQHANQPDETFQAEAOYLQIYAVTPIPEBQE
DOCK3	HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPDDAILQCDAYLQIYAVTPIPDYVD
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGOYIQCFVQPVLDEHP
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGOYIQCFVQPVLDEHP
CONSENSUS	L L Y M F YIQ+ V P D L E

	D	E
CLASP-1	RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN	
TRG	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH	
KIAA1058	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR	
CLASP-2	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR	
CLASP-6	RTILTAIHCFPYVKKRIPFMYQHHTDLNPIEV:HDEMSSKKVAELR	
CLASP-4	RTILTTNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO	
CLASP-3	RTILTTSHAFPIYKTRVNVTHKEEIIILTPIEVAIEDMOKKTQELA	
CLASP-5	NTVLTTMHAFPIYKTRISVIQKEEFVLTPIEVAIEDMOKKTLQLA	
KIAA0716	RTSLYLVSPLPGISRWFVEVEKREVVEMSPLENAIEVLENKNOQLK	
DOCK2	RTSEVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL	
DOCK3	RTTLTLTHSLPGISRWFVEVERRELVEVSPLENAIQVVENKNOELR	
DOCK180	RTSEVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL	
CONSENSUS	RT L FP V + V + P+E AI+ M +L F L L + I	

	F	G
CLASP-1	SLQLKLQGSVSVQVNAGPMAYARAFLEETNAKKYP	DNQV--KILKEIFRQFADACGQALD
TRG	KLQLKLQGSVSVQVNAGPLAYARAFLLDDINTKRYP	DNKV--KILKEVFRQFVEACGQALA
KIAA1055	KLQLKLQGSVSVQVNAGPLAYARAFLLDDINTKRYP	DNKV--KILKEVFRQFVEACGQALA
CLASP-2	KLQLKLQGSVSVQVNAGPLAYARAFLLDDINTKRYP	DNKV--KILKEVFRQFVEACGQALA
CLASP-6	KLQLKLQGSVSVQVNAGPLAYARAFLLDDINTKRYP	DNKV--KILKEVFRQFVEACGQALA
CLASP-3	MLQMVLGSGVGTTVNQGLEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR	
CLASP-4	QLQLKLQGCVSQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFI--QACSTALE	
CLASP-5	MLQMVLGSGVGATVNQGLEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE	
KIAA0716	PLTMCLNGVIDAAVNGGVSRYQEAFVKEYILSHPEEDGEKIARLRRLMLEQAQILEFGLA	
DOCK2	PLSMLLNGIVDPVAVMGGEAKYEKAFFTEEYVRDHPEEDQDKLTHLKDIAWQIPFLGAGIK	
DOCK3	LLSMCLNGVIDAAVNGGIARYQEAFDDKYINKHFGDAEKITQLKELMQEQVHVLGVGLA	
DOCK180	PLSMLLNGIVDPVAVMGGEAKYEKAFFTEEYVRDHPEEAHEKIEKLKDIAWQIPFLAEGIR	
CONSENSUS	L M L+G V VN G Y AFL + + P L+	L
	L I V V F +	I

DOCK1=KIAA1009
DOCK3=KIAA0299
CLASP1variant=KIAA1055

ref 1.1



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1          31
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61          91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121        151
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181        211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241        271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301        331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361        391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421        451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu
          ↓
461        511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541        571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601        631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661        691
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721        751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

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611

841
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn
ref 3.1

1081
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG

1681	1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG	GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu	asp his ser tyr leu pro val gly ser val
1741	1771
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG	GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu	glu glu ser val val ser glu asp thr leu
1801	1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC	CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly	gln tyr phe thr glu ser gly leu val gly
1861	1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC	ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser	thr gly gly leu tyr glu thr val asn glu
1921	1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA	GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu	ala his arg glu phe arg lys leu thr leu
1981	2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC	AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp	ser ile val asn lys asp his lys arg met
2041	2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT	GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe	gly ser lys phe gly asp leu asp glu gln
2101	2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC	AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr	lys leu pro glu ile ser his arg leu glu
2161	2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA	TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu	phe val glu val ile lys asp ser thr pro
2221	2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG	GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys	ala tyr ile gln ile thr phe val glu pro
2281	2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG	GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg	val thr tyr phe glu lys asn phe asn leu
2341	2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC	CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr	leu glu gly arg pro arg gly glu leu his
2401	2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC	ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr	thr met his ala phe pro tyr ile lys thr
2461	2491
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT	GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe	val leu thr pro ile glu val ala ile glu

↓
ref 4.1

2521
 GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
 asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2551
 2581
 AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
 lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2611
 2641
 GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
 glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2671
 2701
 AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
 asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

2731
 2761
 AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
 asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2791
 2821
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2851
 2881
 CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2911
 2941
 TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
 cys glu thr gln leu ser gln gly ser OCH
 ↓ ref 5.1

3001
 3031
 CCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

3061
 3091
 GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

3121
 3151
 TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181
 3211
 GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241
 3271
 AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301
 3331
 TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361
 3391
 AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421
 3451
 TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA
 3541 3571
 ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA
 3601 3631
 CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG
 3661 3691
 CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG
 3721 3751
 CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA
 3781 3811
 AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT
 3841 3871
 CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT
 3901 3931
 TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT
 3961 3991
 GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA
 4021
 AAC TCG

References

BAC sequences of Human CLASP 5

Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC
 TATTTCAATTTAACTAGCTCAGTTTAATCATGTATTTTCTATAAAGGTTAGTCTTATTAAT
 TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC
 ACTAGCTAAGAATTAACAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA
 TCAGGTTAAGTAAAGCCAAGAATCCAATAAGCCCTATGAAATTTAGAAACTCATAGAA
 AAGTCTCAAATCTTCTTGTCTGACATTAGCCAATTGTTATATTATGCAAATAGAGGATT
 NCAAGTAAATAAGTTTGGAACCTGTTTACCAGGTTTTTGCAGCAGNCCTCTAAGAGCTT
 AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
 TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA
 GNCTCTTTAGGCCTNTANTAANTAGAATCTATATGGATTCGTGTTCTGTCNGCAAGNAG
 TGCCTATGAAA

Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 560-580 of the cDNA.

Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCCGCGTTCAGCATGTTGTACTGCTTATAGGGCTGAAGGGAGGCACG
ATTGGGGGATGGAGGCCAGGGAAGAAGTCAAGCAACAGAAAAATTTGAGGCTTAACA
GTCAAGCAACAGAAAAATTCAAAGTGTTCTCTTAAATACCATGACTGTACATCACTG
CTAGGCTGGAGATCTATTGCCAGTAGCCCTGCCTTCCCTAGGCAGGGGAAGCTGTGTT
CTTTGAGTAGCGCTACTCAGCAAAGAGGCTCACCTGGGGCAGTATTTGAGCTAGGCTT
TCAGCCACCGTATCTGAGTACCTCTGTCTTANGAGCAGTGTGGCCTGGTGATCACCCCT
GGGCCTTGATCATGCGTGCTGCAATCCCAGTGATACAAAGAGGCTTTCATGCTGCTAA
GATCTCCAAGTATTTCTCCTTCGTGCTGGGCAGCAGAGGGTTAGACTTNCAGGGGAGA
AGGAAACTGGCTGGGTGCCATGAATAANCTTGCTGTTCAAGANTTAACCTTCTTTGTTAC
ATAAGNGCAAAGGTATAACATAAAGGGNCATGAACTGCTCAACNAAATTNATCAAAT
CCATGTTTGTGGGAGTTCTTTTGTNATNGGAAGTTTAACCCCTAA

Ref 3.1

Sequence of BAC13 using primer C5S3, which spans nucleotides 1086-1105 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCCNGCTCTTTTTGGCAANGTAANCTTGGGATGCTTGTTTTCTTCCTCTTAATTAAGAG
NAAGANTTTTTTTAGCTTCATACTTCTCTCTTCAGGGGGACCAAAAGTCACAGAGCATA
TTAAGTGGCANAACCCCNAAAGGTCTTAAGTCTTCCTAGGAAGAAAGCAGATGCCCTGA
TTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGNGGA
CCTAACTCTAGAAAGTTTAAAANGGCCATTTGCTGAAGGGCTATGACATGAGAACAGA
GATCAACTGAGTGACTTAGCAANTTCACTCTTTCTCTGTAANACCTCTGGTGAGTGAGA
NTAAATCCTNTATGTGACGCCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN
GAAGGNCAGAAATGAATTTCTCACCGCCNGAGGAATGAGGATTATNCTGGGGGGACA
TGCANAAATATTNNNCCCCCNATTTATTNATTTATTTATTTTTGAGACNGAGTNTCGNT
CTAATCGCCCCCAGGCTGGNAGGTGGNAGGTGGTTCCCATCTTNAANCTTANNTNGGA
AGGNCCTCTTTGNGCCCCNNGGGGGGNGNAAAGNGAATTCCCTAAATGCCTNCANNCCC
CTCCCTGGANGTTATTTGGGGGNNTTNTAAAGGGCNGTGGCNG

Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 2196-2205 of the cDNA. Exon sequence is underlined and represents nucleotides 2225-2231.

ACAAAAACTAACCATCANTCTCTAAATCCCAACAANCTTTTTTTAAGAATACCTAANG
AGCTCAACNAGGGGGGACTNTCCAANGCACTTAAATGCAGNCAAACNACNCCNNCAAG
AGNGGCAACTACTAATGGGGCANATCTNAAAGAAAATATAGNCAAAGGNNGGAATCA
TAATAGGAGCNAAGCACTTANGAAGCAGCAACTGGGGAGCTGGGAAGCTGNATNAGGNG

TTCCTANNNTAGAGANGAGANAACCTGGGGACATGGGAAGAGGNAAGCGAAGGGTTCA
AGGGGANGNAAGCGAGCAGANNCCAGGGNCTCANACTNGNGGGGNNTGGGGGGNTN
CTGNNNCCCTACNCTTNGNANGAACAGNGNNGTTGANNTGGCTTTNGANTA

Ref 5.1

Sequence of BAC13 using primer 122047F1, which spans nucleotides 3537-3556 of the cDNA.

Exon sequence is underlined and represents nucleotides 3000-3492. This region does not contain a
intron in this region

CCANNAGATTNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT
ACTTCTACAAGTTTGCCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG
TGGATAATTNTTCCATTTTTCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT
GGGCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTTGGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGTACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCTTCTTNCAAGGGTTNCTAGGGCC

Figure
Multiple sequence alignment of Human CLASP proteins with intron/exon borders
indicated by a vertical line. Numbers in right margin correspond to References

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLILLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLILLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLG YQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLG YQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSI SLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A I I H V V A Q G L E S H L R S Y V K Y A Y K A E P Y V A S E Y H T V H E E L T T I L K P S A D F L T S N
 KIAA I I H V V A Q G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T T I L K P S A D F L T S N
 rat
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K V V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N P M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G --- S V R --- E
 HC5

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D E K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 rat
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S --- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S --- M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V I V S L R L D F L
 HC5

HC2A R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 rat
 HC4 Q T I C N H E H Y I P L N L P M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S I E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D P L T P S E S --- T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S --- V P F
 HC5 --- M N A D T A P T S P C P S I S --- S Q S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S
 HC3 R Q Q H Y L A G L V L T E L A V I L D P A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G L L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A M P N S A S R D E F P C G --- F T S P --- A N --- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D P Y E S E --- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T

LRTS

2.1

2.1

2.1

2.1

2.1

3.1

2.1

2.1

		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLLSEAAMCYVHV
HC4	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLLSEAAMCYVHV
HC1	ATAQMKEHENDPEMLVDLQYSLANSYASTPELRRTWLE	SMARIHARNGLLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSDDLRLTWL	QNMAGKHSERSNHAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASDDLRLTWL	QNMAEKHTKKKQYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYLTRKGV-----		FRQGCTAFRUITPN
KIAA	TALVAEYLTRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRUITPN	
rat	TALVAEYLTRKEAD-----	LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRUITPN	
HC4	AALVAEFLHRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYLKRKGYNKVEKIQTASLLSEDPHPCDSNSLLTTPSGGSMFSGMWPFLSITPN		
HC3	AALVAEYLSMLED-----		RKYLPGVCVTFQNISSN
HC5	AALVAEYLSMLED-----		HSYLPVGSVSFQNISSN

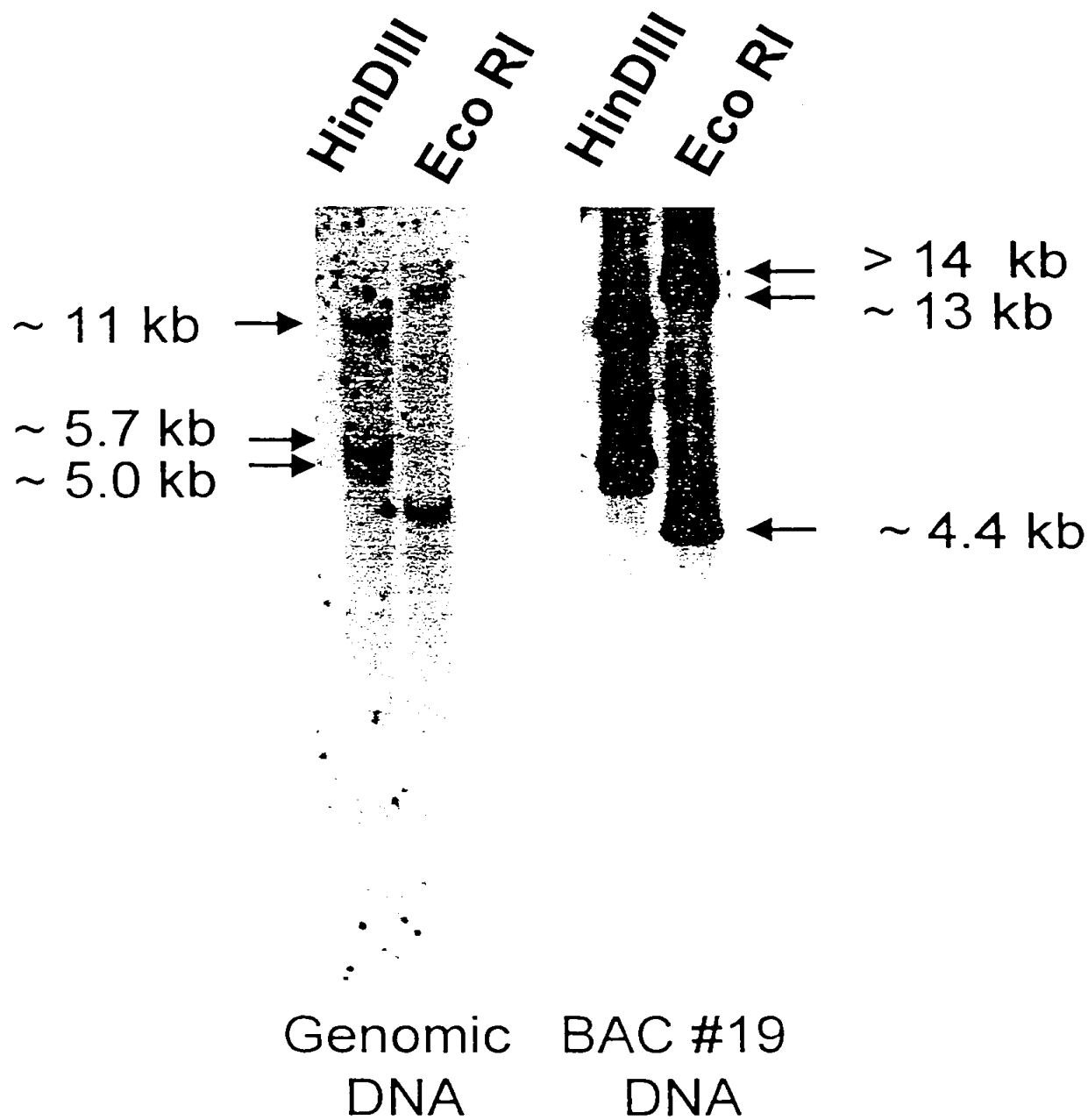
		ITAM
HC2A	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI
rat	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAERYETISEISKLI GPI
HC1	IKKEGAAKEDSGMHD-----	TPYNEINILVEQLYMCGEFLWKSERYELIADVNKPI IAV
HC3	VLEESAVSDDVVS PDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLPI	
HC5	VLEESVVSDDVVS PDEEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPI	

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRDFERLAHL YDTIHRAYSKYTEVMHSGRLLGTYFRVAFFGQAAQYQFTDSETDVE			
rat	SMKSGGTLETTHLYDTIHRFPYSKYTEVITR-----	A-----	AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLLG-----		TFFRVAFYGG	
HC1	FEKQDFKKLSDLIYDIHRSYLKVAEVDNSEKRLFG-----		FYYRVAFYGG	
HC3	HEANRDAKKLSTIHGKLQEAFSKIVHSTGWERMFG-----		TYFRVGFYGG	
HC5	LEAHREFRKLTLTHSKLQRAFDSIVNKH--KRMFG-----		TYFRVGFYGG	

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPPLSEISQRLKLIYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
KIAA	GFFEDEDGKEYIYKEPKLTPPLSEISQRLKLIYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
rat	GFFEDEDGKEYIYKEPKLTPPLSEISQRLKLIYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
HC4	SFFEEDGKEYIYKEPKLTGLSEISLRVLKLIYGEKFGTENVKI IQDSKVNKELDPHYA	
HC1	GFFEEDGKEYIYKEPKLTGLSEISQRLKLIYADRFGADNVKI IQDSNKNVNPKDLDPHYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEAFYGEFGEDEVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGEFGEDEVVEVIKDSNPVDKCKLDPNKA	

	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTVKPYFDDKELTERKTEFERNHNSIRFVFEAPYTLGSKKQGCIEEQCKRRTILTT
HC1	YIQVTVVTPFFEEKEIEDRKTD FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3	YIQVTVVTPFFDYEMKDRITYFDKNYNLRRFMCTPFTLDGRAHGEHQFKRRTILTT

4.1



-111

CGGTAACCGCCATTTTGTCTCCTGTAACAATTTACGCGCCGTGTAAGTGTGAATCTTTCAAAGCCTCAGTTTTATGACC
CTGTGGAGCCAGTGGACTTTGAAGGACTTCTG -1

1/1	31/11
ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG	CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT
Met thr his leu asn ser leu asp val gln	leu ala gln glu leu gly asp phe thr asp
61/21	91/31
GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG	GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG
asp asp leu asp val val phe thr pro lys	glu cys arg thr leu gln pro ser leu pro
121/41	151/51
GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC	AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG
glu glu gly val glu leu asp pro his val	arg asp cys val gln thr tyr ile arg glu
181/61	211/71
TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA	AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT
trp leu ile val asn arg lys asn gln gly	ser pro glu ile cys gly phe lys lys thr
241/81	271/91
GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT	CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG
gly ser arg lys asp phe his lys thr leu	pro lys gln thr phe glu ser glu thr leu
301/101	331/111
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC	CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG
glu cys ser glu pro ala ala gln ala gly	pro arg his leu asn val leu cys asp val
361/121	391/131
TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC	TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG
ser gly lys gly pro val thr ala cys asp	phe asp leu arg ser leu gln pro asp lys
421/141	451/151
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT	GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG
arg leu glu asn leu leu gln gln val ser	ala glu asp phe glu lys gln asn glu glu
481/161	511/171
GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC	TTT GGC CTT TAC CCA TCA GTG GAC GAG GAG
ala arg arg thr asn arg gln ala glu leu	phe ala leu tyr pro ser val asp glu glu
541/181	571/191
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA	TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA
asp ala val glu ile arg pro val pro glu	cys pro lys glu his leu gly asn arg ile
601/201	631/211
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG	ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT
leu val lys leu leu thr leu lys phe glu	ile glu ile glu pro leu phe ala ser ile
661/221	691/231
GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG	ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC
ala leu tyr asp val lys glu arg lys lys	ile ser glu asn phe his cys asp leu asn
721/241	751/251
TCT GAC CAG TTC AAA GGA TTT CTG CGA GCT	CAC ACG CCT TCA GTG GCC GCA TCA AGT CAG
ser asp gln phe lys gly phe leu arg ala	his thr pro ser val ala ala ser ser gln
781/261	811/271
GCG AGA TCT GCA GTC TTC TCA GTC ACC TAC	CCG TCC TCA GAC ATC TAC CTG GTA GTC AAG
ala arg ser ala val phe ser val thr tyr	pro ser ser asp ile tyr leu val val lys
841/281	871/291
ATT GAA AAA GTC CTG CAG CAG GGA GAT ATT	GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC
ile glu lys val leu gln gln gly asp ile	gly asp cys ala glu pro tyr thr val ile
901/301	931/311
AAA GAA AGT GAT GGT GGA AAG AGT AAA GAA	AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA
lys glu ser asp gly gly lys ser lys glu	lys ile glu lys leu lys leu gln ala glu

1021/341

TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG
 ser ser phe phe asn val ser thr leu glu
 1081/361
 GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA
 gly arg ser pro val gly glu arg arg thr
 1141/381
 GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA
 ala leu ser leu glu glu asn gly val gly
 1201/401
 AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC
 ser ser phe phe lys gln glu gly asp arg
 1261/421
 GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG
 ala asp tyr lys arg ser ser ser leu gln
 1321/441
 AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC
 arg leu glu ile ser thr ala pro glu ile
 1381/461
 CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA
 pro val lys pro phe pro glu asn arg thr
 1441/481
 ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG
 thr arg glu val tyr val pro his thr val
 1501/501
 AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA
 arg leu asn phe val asn lys leu ala ser
 1561/521
 ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG
 met cys gly glu asp ala ser asn ala met
 1621/541
 GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT
 glu phe leu gln glu val tyr thr ala val
 1681/561
 GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG
 glu glu val lys ile lys leu pro ala lys
 1741/581
 TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA
 phe tyr his ile ser cys gln gln lys gln
 1801/601
 TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT
 ser trp leu pro ile leu leu asn glu arg
 1861/621
 GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC
 ala leu glu lys leu pro pro asn tyr ser
 1921/641
 AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT
 asn pro pro ile lys trp ala glu gly his
 1981/661
 GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC
 val ser ser val his thr gln asp asn his
 2041/681
 CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC
 leu glu ser gln val thr phe pro ile arg
 1051/351
 AGG GAG GTA ACT GAT GTG GAC TCT GTG GTT
 arg glu val thr asp val asp ser val val
 1111/371
 TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA
 leu ala gln ser arg arg leu ser glu arg
 1171/391
 TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT
 ser asn phe lys thr ser thr leu ser val
 1231/411
 CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA
 leu ser asp glu asp leu phe lys phe leu
 1291/431
 AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA
 arg arg val lys ser ile pro gly leu leu
 1351/451
 ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG
 ile asn cys cys leu thr pro glu met leu
 1411/471
 CGC CCG CAC AAA GAG ATT TTG GAA TTT CCA
 arg pro his lys glu ile leu glu phe pro
 1471/491
 TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG
 tyr arg asn leu leu tyr val tyr pro gln
 1531/511
 GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT
 ala arg asn ile thr ile lys ile gln phe
 1591/531
 CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT
 pro val ile phe gly lys ser ser gly pro
 1651/551
 ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT
 thr tyr his asn lys ser pro asp phe tyr
 1711/571
 CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC
 leu thr val asn his his leu leu phe thr
 1771/591
 GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT
 gly ala ser val glu thr leu leu gly tyr
 1831/611
 CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT
 leu gln thr gly ser tyr cys leu pro val
 1891/631
 ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG
 met his ser ala glu lys val pro leu gln
 1951/651
 AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT
 lys gly val phe asn ile glu val gln ala
 2011/671
 CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC
 leu glu lys phe phe thr leu cys his ser
 2071/691
 GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG
 val leu asn gln lys ile ser glu met ala

2161/721

GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
 val leu phe leu his leu val leu asp lys leu phe gln leu ser val gln pro met val
 2221/741

ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
 ile ala gly gln thr ala asn phe ser gln phe ala phe glu ser val val ala ile ala
 2281/761

AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
 asn ser leu his asn ser lys asp leu ser lys asp gln his gly arg asn cys leu leu
 2341/781

GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
 ala ser tyr val his tyr val phe arg leu pro glu val gln arg asp val pro lys ser
 2401/801

GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
 gly ala pro thr ala leu leu asp pro arg ser tyr his thr tyr gly arg thr ser ala
 2461/821

GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
 ala ala val ser ser lys leu leu gln ala arg val met ser ser ser asn pro asp leu
 2521/841

GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
 ala gly thr his ser ala ala asp glu glu val lys asn ile met ser ser lys ile ala
 2581/861

GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
 asp arg asn cys ser arg met ser tyr tyr cys ser gly ser ser asp ala pro ser ser
 2641/881

CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
 pro ala ala pro arg pro ala ser lys lys his phe his glu glu leu ala leu gln met
 2701/901

GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
 val val ser thr gly met val lys ser met ala gln his val his asn met asp lys arg
 2761/921

GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
 asp ser phe arg arg thr arg phe ser asp arg phe met asp asp ile thr thr ile val
 2821/941

AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
 asn val val thr ser glu ile ala ala leu leu val lys pro gln lys glu asn glu gln
 2881/961

GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
 ala glu lys met asn ile ser leu ala phe phe leu tyr asp leu leu ser leu met asp
 2941/981

CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
 arg gly phe val phe asn leu ile arg his tyr cys ser gln leu ser ala lys leu ser
 3001/1001

AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
 asn leu pro thr leu ile ser met arg leu glu phe leu arg ile leu cys ser his glu
 3061/1021

CAT TAC CTC AAT CTG AAC CTT TTT TTT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
 his tyr leu asn leu asn leu phe phe met asn ala asp thr ala pro thr ser pro cys
 3121/1041

CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
 pro ser ile ser ser gln asn ser ser ser cys ser ser phe gln asp gln lys ile ala
 3181/1061

AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
 arg ser thr val leu thr asp gln tyr arg gln gln his phe leu thr gly leu leu phe

2191/731

CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
 leu phe gln leu ser val gln pro met val
 2251/751

TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
 phe ala phe glu ser val val ala ile ala
 2311/771

AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
 lys asp gln his gly arg asn cys leu leu
 2371/791

CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
 pro glu val gln arg asp val pro lys ser
 2431/811

AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
 ser tyr his thr tyr gly arg thr ser ala
 2491/831

CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
 arg val met ser ser ser asn pro asp leu
 2551/851

GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
 val lys asn ile met ser ser lys ile ala
 2611/871

TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
 cys ser gly ser ser asp ala pro ser ser
 2671/891

CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
 his phe his glu glu leu ala leu gln met
 2731/911

GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
 ala gln his val his asn met asp lys arg
 2791/931

CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
 arg phe met asp asp ile thr thr ile val
 2851/951

TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
 leu val lys pro gln lys glu asn glu gln
 2911/971

TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
 phe leu tyr asp leu leu ser leu met asp
 2971/991

TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
 tyr cys ser gln leu ser ala lys leu ser
 3031/1011

GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
 glu phe leu arg ile leu cys ser his glu
 3091/1031

AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
 asn ala asp thr ala pro thr ser pro cys
 3151/1051

TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
 cys ser ser phe gln asp gln lys ile ala
 3211/1071

CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
 gln gln his phe leu thr gly leu leu phe

3301/1101
 GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA
 ala val ser ala ile his ser leu leu ser ser his asp leu asp pro arg cys val lys
 3361/1121
 CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT
 pro glu val lys val lys ile ala ala leu tyr leu pro leu val gly ile ile leu asp
 3421/1141
 GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC
 ala leu pro gln leu cys asp phe thr val ala asp thr arg arg tyr arg thr ser gly
 3481/1161
 TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA
 ser asp glu glu gln glu gly ala gly ala ile asn gln asn val ala leu ala ile ala
 3541/1181
 GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
 gly asn asn phe asn leu lys thr ser gly ile val leu ser ser leu pro tyr lys gln
 3601/1201
 TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
 tyr asn met leu asn ala asp thr thr arg asn leu met ile cys phe leu trp ile met
 3661/1221
 AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
 lys asn ala asp gln ser leu ile arg lys trp ile ala asp leu pro ser thr gln leu
 3721/1241
 AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG
 asn arg ile leu asp leu leu phe ile cys val leu cys phe glu tyr lys gly lys gln
 3781/1261
 AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG
 ser ser asp lys val ser thr gln val leu gln lys ser arg asp val lys ala arg leu
 3841/1281
 GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA
 glu glu ala leu leu arg gly glu gly ala arg gly glu met met arg arg arg ala pro
 3901/1301
 GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT
 gly asn asp arg phe pro gly leu asn glu asn leu arg trp lys lys glu gln thr his
 3961/1321
 TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
 trp arg gln ala asn glu lys leu asp lys thr lys ala glu leu asp gln glu ala leu
 4021/1341
 ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
 ile ser gly asn leu ala thr glu ala his leu ile ile leu asp met gln glu asn ile
 4081/1361
 ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
 ile gln ala ser ser ala leu asp cys lys asp ser leu leu gly gly val leu arg val
 4141/1381
 CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA
 leu val asn ser leu asn cys asp gln ser thr thr tyr leu thr his cys phe ala thr
 4201/1401
 CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT
 leu arg ala leu ile ala lys phe gly asp leu leu phe glu glu glu val glu gln cys
 4261/1421
 TTC GAC CTA TGT CAC CAA GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
 phe asp leu cys his gln val leu his his cys ser ser ser met asp val thr arg ser
 4321/1441
 CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT
 gln ala cys ala thr leu tyr leu leu met arg phe ser phe gly ala thr ser asn phe

4441/1481

TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC
 phe asn glu glu his leu arg arg ser leu arg thr ile leu ala tyr ser glu glu asp
 4501/1501
 ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT
 thr ala met gln met thr pro phe pro thr gln val glu glu leu leu cys asn leu asn
 4561/1521
 AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG
 ser ile leu tyr asp thr val lys met arg glu phe gln glu asp pro glu met leu met
 4621/1541
 GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG
 asp leu met tyr arg ile ala lys ser tyr gln ala ser pro asp leu arg leu thr trp
 4681/1561
 CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC
 leu gln asn met ala glu lys his thr lys lys lys cys tyr thr glu ala ala met cys
 4741/1581
 CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC
 leu val his ala ala ala leu val ala glu tyr leu ser met leu glu asp his ser tyr
 4801/1601
 CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG
 leu pro val gly ser val ser phe gln asn ile ser ser asn val leu glu glu ser val
 4861/1621
 GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC
 val ser glu asp thr leu ser pro asp glu asp gly val cys ala gly gln tyr phe thr
 4921/1641
 GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA
 glu ser gly leu val gly leu leu glu gln ala ala glu leu phe ser thr gly gly leu
 4981/1661
 TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA
 tyr glu thr val asn glu val tyr lys leu val ile pro ile leu glu ala his arg glu
 5041/1681
 TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC
 phe arg lys leu thr leu thr his ser lys leu gln arg ala phe asp ser ile val asn
 5101/1701
 AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT
 lys asp his lys arg met phe gly thr tyr phe arg val gly phe phe gly ser lys phe
 5161/1721
 GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG
 gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu pro glu
 5221/1741
 ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG
 ile ser his arg leu glu ala phe tyr gly gln cys phe gly ala glu phe val glu val
 5281/1761
 ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG
 ile lys asp ser thr pro val asp lys thr lys leu asp pro asn lys ala tyr ile gln
 5341/1781
 ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT
 ile thr phe val glu pro tyr phe asp glu tyr glu met lys asp arg val thr tyr phe
 5401/1801
 GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG
 glu lys asn phe asn leu arg arg phe met tyr thr thr pro phe thr leu glu gly arg
 5461/1821
 CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC
 pro arg glu glu leu his glu gln tyr arg arg asn thr val leu thr thr met his ala

4471/1491

4531/1511
 4591/1531
 4651/1551
 4711/1571
 4771/1591
 4831/1611
 4891/1631
 4951/1651
 5011/1671
 5071/1691
 5131/1711
 5191/1731
 5251/1751
 5311/1771
 5371/1791
 5431/1811
 5491/1831

5581/1861

ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG
ile glu val ala ile glu asp met lys lys

5641/1881

CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG
gln glu pro pro asp ala lys met leu gln

5701/1901

GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA
val asn gln gly pro leu glu val ala gln

5761/1921

AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG
lys leu tyr arg his his asn lys leu arg

5821/1941

GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC
gly glu ala val glu lys asn lys arg leu

5881/1961

GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA
glu leu lys lys asn tyr asn lys leu lys

5941/1981

ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA
ile pro glu leu tyr lys pro ile phe arg

6001/2001

AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

5611/1871

AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
lys thr leu gln leu ala val ala ile asn

5671/1891

ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
met val leu gln gly ser val gly ala thr

5731/1911

GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
val phe leu ala glu ile pro ala asp pro

5791/1931

TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
leu cys phe lys glu phe ile met arg cys

5851/1951

ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
ile thr ala asp gln arg glu tyr gln gln

5911/1971

GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
glu asn leu arg pro met ile glu arg lys

5971/1991

GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
val glu ser gln lys arg asp ser phe his

6031/2011

TTG TCA CAG GGC AGC TAA
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAGCCATCTTCATTTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAATGGGACATT
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
CCCAAATGGACTCTGACCAGATTTTGGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
TTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCCATC
TGAGAGATGATTTCCCTCTGGCCCATATTTGAATTTATTGGAGTAACCTCAAATTGCCTGAGGAAAAATGGAAAAATTATCC
ACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACCTTGTAGGAGTACGAAACATTTTCAATAAAT
CTACAAAGGGAAGCCTTACTACAATTCCAAAAATCATCATGTTGGAAATTTGGGAGGAGATTATTTGTGAACCTTGTTAC
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT
CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTC
TCTGGGACCAAGTTTCTTTTTATAAAGCAATAATATCTCTGTTTTCATTTTCAGAACATTGTGCTGTCTGTGACATATGT
ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
AGAATTAAATTATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAA
AAAAAAAAAAAACTCG

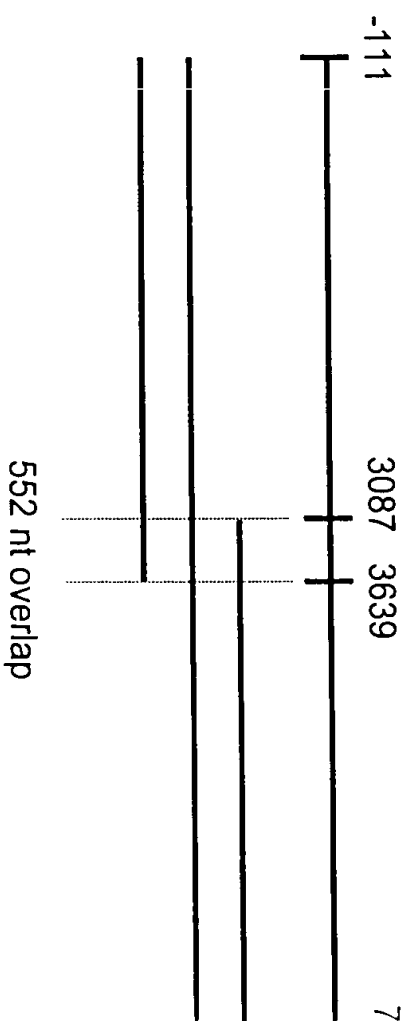
A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

nucleotide numbering
as in Figure 6A



1st partial exon (nucleotides 3793 to 3952)

CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCATGAGGCTAG
AGTTCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTT
TTTATGAATGCTGATACTGCTCCAACATCTCCTTGTCTTCCATATCTTCCCAG
GTAATAAAAGAATTATTAACTAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5948)

GTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT
TCCAGGACCAGAAGATCGCCAGCATGTTTCGATCTGACTTCCGAGTACCGCCA
GCAGCACTTCCTCACCGGGCTCCTCTTCACAGAACTGGCTGCTGCCCTGGATG
CCGAAGGGGAAGGGTATGTTTCTGGCATTTAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)

CATAACCTCTTGATTCTGTGTTGTGCCAACAGAAATCAGCAAAGTACAAAGG
AAAGCTGTCAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCAC
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATCGCCGCCCTTTACCTACCTTTA
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG
CCCTTCTGTTTTCTTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)

TGTTTGACTTGACATCACAAACGATGTTTTATTGCAGTTGCAGATACTCGCA
GATACCGCACCAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA
ACCAGAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG
TGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 19281 to 19463)

TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG
CTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG
CAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT
AAGGTAAGTCTGGAGTGGCACAACTTTATACCAGC

6th exon (nucleotides 19829 to 19958)

CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGAGTTCT
GACAAAGTCAGTACCCAAGTCCTGCAGAAGTCAAGGGATGTCAAGGCCCGG
CTGGAAGAGGCTTTGCTGCGTGGGGAAGGGGCCAGAGGGGAGATGATGCGC

7th exon (nucleotides 20928 to 21015)

TCAAATTCCTATCATGCATTTCTTAACTCCTAGGGAACGACCGATTTCAGGC
CTAAATGAAAATTTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCT
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCTACTTTTACCT

8th exon (nucleotides 25765 to 25861)

GCTTTAATTTGACCTCTTGTTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAG
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGA
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTG

9th exon (nucleotides 27242 to 27376)

GGATTCAATGATGCTGTTCTTCCATTCCCCAGGCCGAGCTCGGCTCTGGACTG
TAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGTGAATTCTCTGAAC
TGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT
CATCGCCAAGGTAAACTTGGGATGCTTGTTTTCTTCCTCTTAATT

10th exon (nucleotides 28582 to 28734)

AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGAGACTTACTCTTCG
AAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTG
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCTTTACCTC
CTCATGAGGTTTCAGTTTTGGAGCCACCAGTGTAAGAGTTCAAACCAGCTGAG
TGACCTGGAATCAG

11th exon (nucleotides 31046 to 31204)

TTACTTCATCTTTTTTTTTTTTTCACTGATGCAGAAATTTTGCAAGAGTAAAGA
TGCAAGTAACCATGTCCCTGGCATCTTTGGTGGAAGAGCACCAGACTTTAA
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG
GACACAGCCATGCAGATGACTCCTTTCCACCCAGGTACACCGAAGCACAT
ACCTTGTCTCATGCATGAGT

12th exon (nucleotides 32755 to 32855)

AGCTAAGATTATTTTGAGGCTTACACTTTTTGCAGGTGGAGGAACTTCTCTGT
AATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAATTCAGGAAG
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACTCA
AGGGACACCATTT

13th exon (nucleotides 33663 to 33855)

TCCTCAAACTACTTCTCACTCAATCTGTCTTCAGAAATTGCCAAGAGTTACCA
GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACAC
ACCAAGAAGAAGTGCTACACGGAGGCTGCCATGTGCCTGGTGCACGCCGCTG
CGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCCG
GGCAGTGTGAGCTTCCAGGTAGGGTGTGTGCAGCTTTCCCTTAGAGCAGTG
GTTC

CTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTGAGGACACCCTGTACCTGACGAGGATGGGGTG
TGCGCAGGCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG
CCGCGGAGCTCTTCAGCACGGTCAGTGCCAGAGGGCATCCCGGGGCCTGGC
C

15th exon (nucleotides 40166 to 40297)

AATTCTCTCTGATGCTCTTCTCCTCTTTCCAAGGGAGGCTTATATGAGACAGT
TAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCGAGAATTC
CGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCCTGGCTGGCAGGTCTTGTTAC

16th exon (nucleotides 40755 to 40889)

TAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAATGTTTGGAA
CCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)

AACCTTTATAAACTGTTGGTTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT
GGTGCAGAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACAAGGTATACAAAAATTTACAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)

TCTTCTCCCTCCGTGCCTTTTCCCCCTTAGGCCTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGA
AGAATTTCAACCTCCGGAGGTTTCATGTACACCACCCCGTTACCCCTGGAGGG
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC
CACTATGCACGCCTTCCCCTACATCAAGACCAGGATCAGCGTCATCCAGAAG
GAGGAGGTAATGCACCCAAGGGATTGGCCACCACTGGATGAGT

19th exon (nucleotides 48664 to 48807)

ACAGTGA CTTCCTATGTTTACGTCTCATGTT CAGTTTGT TTTGACACCGATTG
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT
TAACCAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCT
GTGGGAGCTACTGTAAATCAGGTAAGCAAACCAGAGGTGGCAGCTCCT

20th exon (nucleotides 50892 to 50998)

TATATTCTTTTTTTTTTTTTTTTTTTTTTTTCCCACCAGGGACCACTGGAAGTAGC
CCAAGTGTTTTTGGCTGAAATTCCTGCTGATCCAAAACCTCTATCGACATCACA
ACAAGTTGAGGTTATGCTTTAAGGAATTCATCATGAGGTAAGAAGGAAAATG
GCTGGGAATTT CAGTAGAG

21st exon (nucleotides 62398 to 62568)

TCAAAAAGAACTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC
GGAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAG
GTAAGAACAGGGCAGAGGAGGCCTCTTCCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)

CCTCCCTCTCTTTTCTTAATTTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA
AATGTGAAACCCAGTTGTACAGGGCAGCTAAGAAAAGCCATCTTCATTTCGT
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC
TGGAAGCTTTGGGATCCCAGGAACCATGGAATTATTCCCAAATGGACTCTGA
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC
ATGACTGCGTATTTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTC
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT
GGAAAAATTATCCACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAG
GCAGGGCAAACCTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA
AGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT
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ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA
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TCTGTCAGCATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG
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ATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA
TTGCAAGCTAAAAAAAAAAAAAAAAAAAAA

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 4642 TCTTACTAATTGAAAAAAAATCTTAGCCATATATGCCATATGGCATGATCCAGATATTAGCTACATGACCATCTTACTGTGAACAGGGAA
 4733 AGATCTGACTCACAAGCAGCAATTCAAATGTATAAACTTTTGTCTCCATCCTGCCAGCAGCTTAAGTCCATAAACTTCCCTGGACTAAG
 4824 CTTACCCTAGGTTCTTTCCACCTTCCCTTCTGACTGCCCCAGGGAGTGGCCAAACCCAGGGGCCAGGCTCACAAAACCATGAAGGATTT
 4915 CTAAGACACTTTAGATGCTCTTAATGAAATATAAAGTGTGCTCCCAGGATACAAATACAGGACAGGAATTACTGAGGACCGGTAAATCTA
 5006 ATACTTCCCTCCCTGACATCATTGTAGTTCCAGGCCAGCAAAAGTCTGACAATGTGCTTAAGCCAAATTGAGAAGTGTAGCTGAGGCCGG
 5097 GCACGGTGGCTCACATTTGTAATCCAGCATCTTCGGAGGCCAAAGGGAGTGGAAATCTTGAGGCAGGAGTTACCAGCCTGACCAACATGA
 5188 TGAAAACCTCATATCTACTAAAAATACAAAATGCATCAGGTGTGGTAGTGTGACTGTAATCCAGCTACTTGGGACGCTGAGGCATGAGAA
 5279 TTGCTTGAACCCGGGAGAGGGAGGTTGCAGTGAGCTGAGACCATGCCACTGCAATCCAGCCTGGGTACAGAGTGACACTCTGTCTTTCAA
 5370 AAAAAAAAAAAAAAAAAAAGAGGTACCTGAGTAAGCAGGGCCTTAAACAAAGGGGCCATTGGTTACAGAGGAATTGCCTGTCTCCAGC
 5461 CCCAGGACTGGGTGAGGTTCTTATTTCTCTGTCCAACCTTTTATGCTAGGATTTTTATCTTCAGCTTTTGATTTGAGGTGGGAAAGGGAGCG
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 5643 ACTCTGTGCTCAGTTTCTTGTCCGCTTATCTGGCACCAGAGTACCTACCTCACTGGGGAGGGCTCACGAAGCCTGGCTGGGGCGAGGA
 5734 CTCAGTAAACACTGGCCATCGCTATTTTCATTCCAGTTCTTGTGGCTCATAAAATGGCTCCTTACGTTCTGTAGAACTCAAGCTCCTGCT
 5825 CCAGCTTCCAGGACCAGAAGATGCCAGCATGTTGATCTGACTTCCGAGTACCGCCAGCAGCACTTCTCACC GGCTCCTCTTCACAGA
 5916 ACTGGCTGCTGCCCTGGATGCCGAAGGGGAAGGGTATGTTTCTGGCATTTAAATGGAAGATGAAGCCAAAAAACAGATGTTCTTTAATA
 6007 AAATTTGCAGTCTAGCTTCTCACACTTGGTAAAAACTCTACTGTAGTTGACCACTTCTGAGGAGTAGAAACATCTGTCTTGAGAATATGG
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 39404 CTTTTCAAGATTCAAGAAATGTCTAATATACTCTCATTTTTCTCAAACCTCAACAAAATGAATTAGAATCCTACTAACTCTTTGGAGGCAT
 39495 ACATTTAGCATCTGGCTAGAGGAGGACCTCTGATGAAATTTAAATATACTAAACTGCCTTTCTGAATTGCTGTTAGTCCCTGCTACCAAA
 39586 CTCTCTCTCTGTTTTTCTTTCTGTTTTGTTTTGTTTTGTTTTGTTTTGAGGACGCTCTTGCTTGTACCCAGGCTGGAGTGCAGT
 39677 GATGCAGCCTTGGCTCACTACAGCCTTGACCTCCTGGGCTCAGCCTCCACCTCAACCGCCCAAGTAGCTGAGGCTACAGGAGCATGCTAC
 39768 CACACCTGGCTGATTTTTTAATTTTTTTGCAGAGATGGGGTCTCCCTATGGTGTCTAGGATGATCTGAACCTCTGGGTTCAAGTGATCTCT
 39859 CTGCCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCCTCAGCCAGTATTTTTTTTTTCCCCGAAAGCTCTTCTCTTAC
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 40041 GTGAAATACTGTGATACAACAATAAATCACTCTCCAGCACATTGTTTGACAATGACCTCTGGTTGCTCTTCTTAAGTTTCCAGTGGATT
 40132 AAATCTCTCTGATGCTCTTCTCTCTTTTCCAAGGAGGCTTATATGAGACAGTTAATGAGGCTACAAGCTGGTCATCCCCATCCTAGAA
 40223 GCGCATCGAGAATTCGGAAGCTGACACTCACTACAGCAAGCTGCAGAGAGCCTTCGACAGCATCGTTAACAAGGTAGCCGGGGAGCCTG
 40314 GCTGGCAGGTCTTGTTACCTGGTGGCAGGCGACCTGTCTACAGATGCTTAGCCATCCTTCTCTCCAGGAGTGAATTTATCTTTAGCAC
 40405 ATTGCTTTTGTCTCTCACCTGTCAAACAGAAAAGGGCTGAAATCTTCTAACAGAGGACCAAAATCCATATGTGAAAACATACAGCTTAA
 40496 TTACTTTTATAACCAGGAAATGTGAGAAATTTTAAAGTGAATTTAAAGAAAGTCCAGAAATCTTTCATGGGATTCTTTTGTGTTATTTCT

[illegible]

B

59151 GAAGGTGTTAGCTAGCTGCTGCTACTTCTGCAACAAAGACTAAGGAGAGTTTACCTGATTTTACCAAAGTTGTCGAGTAGACTTCCCCA
59242 AATTAGCTGTTAGCTTTGGCAGGACTCATCCCACCTCCTGTAGCCTGCCAATGTTATAAACTTGGGCCCTTGAAGTCATCCTGAAACTGATC
59333 TTATTTTACACATGGTGGTAATTGTAACCTGTTAGTTAAGAAGCAATAAAAAAATAAAGGGGTGATATAGATTTCTCAGGATTCAAAGGC
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59515 GATAGGTGAAAATCCAGTTAAGGGAGTTCTTTTCAGATTCTGTGTGAGTTAAATCAAGTCCTTCTTCTATAGCAGGCTAATTCATGATGAA
59606 GCTGTGGTGCTAAGTTTATTTTGCCTAGGCAGGTAGCTCTTCCCTGCCACATGCTATCCTCTTCTCTTGGACTGTCATCCTGAAAATGT
59697 GTTCAGTGTTAAGAGGATTTGATAACAATGTCTGGGTATCTCCATAACTTAGTCCAAATCTGGTACCCTGTTAGGAAAATAATGTAAGCC
59788 ATATTGATCACCACGCTTATTTCATTTGAAGGATAATATAGTTATTACTAATTATTGCGTGTAGGTAACATACAGCCATTATTCTGTCC
59879 CTTAAGGTTTATTGATTGTAGTTTCCCTTGGGTAGAAGAGTACAAAACAAAGGCCAAACTTCATCATGTTTAAATAACGTGATTTTCT
59970 TCTTGGTGTGTACCGTACCGTGCAGGAGACAGGGAAAACACCAGGTTTAAACGGTCCACAAGCCAGATAACCATGATGAGTTCTAAAGATT
60061 TTCTCTGTCTTTAATGTTCTTCAGTTTGTCTATGAGAAGACTGGATATAGCTCTGTGTGTGTTTCATTAGAGGATTATATCTCTCTTCAAC
60152 TCTAGAAAATTACCAGCTGTTATCTCTTTAAATATTGTCTCCCTCTCATTTTCCATTCCCTTGGAGATTCTATTAGATGTGGTTGGATCT
60243 TCCTTATATCTCTATGTTTCTTAACCAATTTTTTCATATTTTTTATTTTTTAAATCTCAITGGTGATTCTCCTTGGATCTGTCATACATTT
60334 ACTTCTCCAATTATGTCTAGTCTATTATTTAACCTTTAACCTTTCCATTGAGTTTTTTGTCTTTTAGCAACTGCATTTTTTTTTTTTTTTT
60425 TTTTTTTTTTTTGGTGAGACAAGGTCTGGTTCTGTCAACCCAGGCTGGAGTGCAGTGGCATGATCTTGGCTCACTGCAACCTCCACCTCCC
60516 AGGCTCAAGCCATCTTCCACCTCAGCTTCCCAAATAGCTGGGACTGCAGTCACCTGCCACCATAACCCAGCTAATTTTTTATATTTTTTGTA
60607 GAGATGGGGTTTTGCCATGTTGCCAGTCTAGTCTTTAACTTGTGAGCTCAGGCAATCCACCACCTTAGCTTCCCAAAGTGTGGGATTA
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61426 TCACTAATCTTGTGTGAGCTTTGAAGCCCCCTCCCCCTCAGCCCATAGACCTATACACAGTCTTAAATCTTAATGGGAGTCTTACTGACA
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62518 GAAAATCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAGGTAAAGAACAGGGCAGAGGAGGCCCTTCTCTGTGGGATAAA
62609 GAGCAGCGCATGGGGCTAGCACCTTGGGGCATGCTCTGCTGCACTTGGGAGCTGCAGAACCTCGAAAGGGTGAAGAGGGTCCCACAGT
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63701 TGTTTTATTATTACTGTTACATTAATTTAACATGCATTTATAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGC
 63792 AGTCAGCCAGAAATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTCTTATGTCACCTCTTGTGTA
 63883 CTATCTATTTTCTCCTCTCTGGGACCAAGTTCTTTTTTATAAAGCAATAATATCTCTGTTTTCAATTCAGAACATTGTGCTGTCTGTCAG
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 64793 CCCTAGTAACCTAGAATATTCTGATTAAATATCCCCCTGCTTTTAGATACCTGTTGTCCATTGGGTTTGTTTTTACAGTCTCTTTTGTA
 64884 CCACAGTGGATACATTTGCTTCATGAGTGCAGGAACCATGTTCACTGCTGCATTCTTACCCCTAGCCCTGCAACAAACACACAAAAGATAC
 64975 CCAATAAATATTTGTTGATTCACTAAATGAATGAATGATGAGTAGGCCCTGCTTCTAGAAGTGCAGTGCCAATAAGAATGTAATGCAAGCCA
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 65248 AATTAACCAAGTGTGGTGGCATGTGCCTGTAGTCCAGCTACTCGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGAGGTTGAGGCTG
 65339 CAGTGAGCCATGATCGTGTCACTGCACTCTAGCCTGGGTGACAGAGTGAGACCCTGTCTCAAAAAATAATCAGCATCATAAAAAGAAACCA
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 66158 CAAGGTCAAGGGTGCAGTTGTCACTATCACATAAGAATCTCATAAAAAATTAAACATGAATATACTGCACAGATCTGATTGGGTTTGTGATG
 66249 CCACACATTGTTTTAAATCCATAATTCTATTCTATAAAGAGTGGTTTCTATGACAAATAGATCGTTTTAAAAACAAACAAACAAACAAAT
 66340 TTAGAGTTGTCAATTGGTAATTGIGGTTGCAAGTATGCTTTCAAAGACCAGAAGCTTTTGTGTTGCTTTGAATGTAATTTTTTTCTTTTTTC
 66431 TTTTTGATACGGAGTCTCACTCTGTTGCCAGGCTGGAGTGCATTGGCACCATCTCAGCTCACTGCAACCTCCACCTCCGTTGGTTCAAGCA
 66522 ATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGTCCACCACCAGCCTGACTAATTTTTGTATTTTAGTAGAGATGGGGTT
 66613 TTACCATGTTGGCCAAGCTGGTCTCAAATTCCTGACCTCAGGTGATCCACCTGCCTCTGCCTCCCAAAGTGCTG

Putative promoter sequence of human CLASP-5

GGAACAATTTCTCTCATGTGTATGGCTCCCTAAAGTGTTGGCTGAGCATTGTCCACATGGGTG
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CATGATTTAAAGGATTCTAGTCAGATACCAGACATCCTCACATAGAGAAAACCTCTGAATGGCTG
GGGAGAAGGAGTCAAATGCCCTGGATCTTTTTCTTGGGCCTCAAAGTCCTCCTTCTGTCATCA
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ACTAAATGCCAGATGTGTGCCAAGTGAGATAAATCTGACAAATGAGATGGTTTGTAAAACCAGC
AGTGAATATTCACCTCCTCTGTGAGAGAGCTCCAGCCCTCCTGTACTCACTTCCTCACACAGCA
CAGCAGCACTCTTGCTGGTTCTGCTGCTTATCTTGAAGAGGTAGGTTACTTTTTGTTTCTACT
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hCLASP4 -----MFPMEDISISVIGRQRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG 41
hCLASP2 -----MLLFPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVKREPSEFWKKRRRTVRRVIQEEFHRFSSQEKPRLLLEPLDYETVIEELEKTYRN 60
      ...:

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHVVNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPKAE EEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQWHVVNYK 120
      ::

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDL DVVFTPKCRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YFDYSGEFROLPNKVVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLQPRECRTEP-GIPKD-EKLD AQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLP SHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG 180
      :: .      : * . : * .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGDERSGPEDSND SRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVR SFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT 239
      : :      . : :      *      : :      . : .

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLAETE QEME EWLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKG PVTACDFDLRSLQPDKRL ENLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE 234
hCLASP2 GVVQNNKVRRF AFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSI FDLRLNLAADSL LPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELK MNDLTYFVLAETESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * : :      . : :      . :

hCLASP4 TAQDDETSS----QGKAENIMASLERSMHP ELMKYGRETEQLNKLSRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEPIERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLDSYLP ELAKSAREAEIK---LKSES RVKLFYLDPD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRILVKCLSLKFEIE 273
hCLASP1 TDGLGDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTNRMERLNLFS LDPD 359
      .      :      : : : : :

hCLASP4 VQRLDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKKISENFYFDLNSEQMKGLLRPHVPPAAITTLARS AIFS I 333
hCLASP2 AQKLD FS----SAEPEVKS-FEEKFGKRILVKCN DLSFNLQCCVAENE EGPTTNVEPFFV 327
hCLASP7 IEPIFGI----LALYDVREKKKISENFYFDI NSDSMKGLLRAGH THPAISTLARS AIFS V 329

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hCLASP4	NLALFDVKNCKISADFHVDLNPSSVREMLWGSSTQLASDGSP---KGSSPESYIHGIAE	390
hCLASP5	TYPSSDIYLVVKIEKVLQOQD----IGDCAEPYTVIKESDG-----GKSKE-KIEKLKL	317
hCLASP3	TYPQDVFLVIKLEKVLQOQD----IGECAEPMIFKEADA-----TKNKE-KLEKLKS	382
hCLASP2	TLSLFDIKYNRKISADFHVDLNFHFSVRQMLATTSPALMNGS-----GQSPSVLKGILHE	381
hCLASP7	TYPSPDIFLVIKLEKVLQOQD----ISECCEPYMVLKEVD-----AKNKE-KLEKLRL	378
hCLASP1	SVALYDLRDSRKISADFHVDLNHA AVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE	479
	. . * : * . : . : : :	
hCLASP4	SQLRYIQOGIFSVTNPHPEIFLVARIEKVLOGNITHCAEPYIKNSDPVKTAQKVHRTAKQ	450
hCLASP5	QAESFCQR-----LGKYRMPFAWAPISLSSFFNVSTLEREVDVDVSVGRSPVGERRTLA	372
hCLASP3	QADQFCQR-----LGKYRMPFAWTAIHLMNIVSSAGSLERDSTEVEISTGERKGSWSERR	437
hCLASP2	AAMQYPKOGIFSVTCPPHDFILVARIEKVLOGSITHCAEPMKSSDSSKVAQKVLKNAKQ	441
hCLASP7	AAEQFCTR-----LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----SEGERRPAWTD RR	429
hCLASP1	EWLKFPKQAVFSVSNPHSEIVLVAKIEKVLGMNIGASGAEPYIKNPDSNKYAQKILKSNRQ	539
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hCLASP4	VCSRLGQYRMPFAWAARPIFKDTQGSLLDGRFSPLYKQDSSKLSSSEDIKLLSEYKKPE	510
hCLASP5	QSRRLSERALSLEENGVSNGFKTS-----TLSSVSSFFKQEGDRLSDEDLFKFLADYKRSS	427
hCLASP3	NSSIVGRRSLERTTSGDDACNLTSFR-PATLTVTNFFKQEGDRLSDEDLKFLADMRRPS	496
hCLASP2	ACQRLGQYRMPFAWAARTLFKDASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPE	501
hCLASP7	---RRGPQ--DRASSGDDACSFSGFR-PATLTVTNFFKQEAERLSDEDLFKFLADMRRPS	483
hCLASP1	FCSKLGKYRRFAWAVRSVFKDNQGNVDRDSRFSPLFRQESSKISTEDLVKLVS DYRRAD	599
	. . : : * : : : * : * : : : : . . .	
hCLASP4	--KTKLQIIPGQLNITVECVVDLSNCITSSYVPLKPF-KNCQNI TVEVEEFVPEM TKY	567
hCLASP5	SLQRRVKSIPGLLRLEISTAPEIINCCLTPEMLPVKPPF-ENRTRPHKEILEFP--TREV	484
hCLASP3	SVLRRLRPITAKLKIDISPAPENPHYCLTELLQVKLYP-DSRVRPTREILEFP--ARDV	553
hCLASP2	K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH	560
hCLASP7	SLRRLRPVTAQLKIDISPAPENPHFCLSPPELLHIKYP-DPRGRPTKEILEFP--AREV	540
hCLASP1	R-ISKMQTIPGSLDIAVDNVPLEHPNCVTSSFI PVKPFNMMAQTEPTVEVEEFVYDSTKY	658
	: : : . * : : : : * : : * : *	
hCLASP4	CYPFTIYKNHLYVYPLQLKYDSQKTFAKARNIAVCVEFRDSDASALKCIYGKPA GSV	627
hCLASP5	YVPHTVYRNLLYVYPQRLNFVN--KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE	541
hCLASP3	YVPNTTYRNLLYIYPQSLNFAN--RQGSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE	610
hCLASP2	TCPYTIYTNHLYVYPKYLKYDSQKSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPV	620
hCLASP7	YAPHTSYRNLLYVYPHSLNFSS--RQGSVRNLAVRVQYMTG-EDPSQALPVI FGKSSCSE	597
hCLASP1	CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYGKPEGPL	718
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hCLASP4	FTTNAYAVVSHHNQNPFEYDEIKIELPIHLHQKHLLFTFYHVSCBINTKGTTKKQDTVE	687
hCLASP5	FLQBYTAVTYHNKSPDFYEEVKIKLPAKLTVNHHLLFTFYHISCO-----KQASVE	595
hCLASP3	FSKBYTAVVYHNRSPDFHEEIKVKLPATLTDHHHLLFTFYHVSCQ-----KQNTLE	664
hCLASP2	FTRSFAA AVLHHQNPEFYDEIKIELPTQLHEKHLLLTFFHVSCDSSKSGSTKKRDVVE	680
hCLASP7	FTREAFTPVYHNKSPDFYEEFKLHLPACVTENHHLLFTFYHVSCOP-----RPGTLE	651
hCLASP1	FTSAAYTAVLHHSQNPDFSDEVKIELPTQLHEKHILFSFYHVTCIDINAKANAKKKEALE	778
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hCLASP4	TPVGFAWVPLLKDGRIITFEQQLPVSANLPPGYLNLNDAESRRQCNVLIKWVDGAKPLLK	747
hCLASP5	TLLGYSWLPILLNERLOTGSYCLPVALEKLPPNYSMHA EKVP LQNPPIKWAEGHKGVFN	655
hCLASP3	TPVGYTWIPMLQNGRLKTGFCLPVSLKPPQAYSVLSPEVP---LPGMKWVDNHKG VFN	721
hCLASP2	TQVGYSWLPPLLKDGRTVTEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVDGKG PLLK	740
hCLASP7	TPVGFTWIPLLQHGRRLTGFCLPVSDQPPPSYSVLTPDVA---LPGMRWVDG HKGVFS	708
hCLASP1	TSVGYAWIPLMKHTQIASQFYNIPIATSLPPNYLSFQDSASGKHGGSIIKWVDG GKPLFK	838

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS	-----GSKEVPGELIKYKLCIHLAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLES	SVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH	-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFFQYCQKTES	-----GAQALGNELVKYKLSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG	-AFFPRLKDTVLSSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK	-----MSQSPTS NFIRSCKNLLNVE	887
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hCLASP4	ETQVMIQFLPVLMLQFLR	-----VLTNMTNTH-----	EDDVP 824
hCLASP5	RLEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQ	FAFESVVAIANSNLHNSKDLSDQHG	775
hCLASP3	QLEPVVRFLLHLLDKLILLVIRPPVIAGQIVNLGQAS	FEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQLFR	-----VLT-RAT-----	QEEVA 816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGA	FEAMAHVVSLVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK	-----VLVQNE-----	EDEIT 916
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hCLASP4	INCTMV-LLHIVSKCHEEGLDS	-----YLRSEFIKYS-----	FRPEKP 860
hCLASP5	RNCLLASVYVHYVRLPEVQRDPVPSGAPTALLDPRS	YHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVRLPNTYPNSSSPG-PGGLGSSVHYAT	MARSAPASLNLNRSRSLNS	899
hCLASP2	VNVTRV-I IHVVAQCHEEGLES	-----HLRSYVKYA-----	YKAEPY 852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP	---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIIVAKCHEEQLDH	-----SVQSYIKFV-----	FKTRAC 952
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hCLASP4	SAPQAQLIH	-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC	SRMSYYCSGSSDAPSSPA	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGG	PKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH	-----EELTKSMITILKPS-----	875
hCLASP7	SNPDLAVAGSVDDDEVSRILASKLLHEELA-LQ	-----	915
hCLASP1	KE--RPVH	-----EDLAKNVTGLLKS	972
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hCLASP4	-----ADFLSINKLLKYS-----	-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----	-----MVVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLPTKKLFHEELALQ	WVVCSSGVSRESALQAWFFFLMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----	-----WFFFDVLIKSM	899
hCLASP7	-----WVVSSAVREAILQHA-----	-----WFFFLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----	-----WFFFAIILKSM	995
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	Cadherin Cleavage		
hCLASP4	ATYLLEENKIKLIRGQRFETYYHVLHSLLLAIIPHVT	IRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEHRTRESDRFMDDITIVNVVTSE	IAALLVKPQKENEQAEMNISLAF	970
hCLASP3	VHHLYFNDKLEAHRKSRFERFMDDIAALVSTIAS	DIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQHLENSKVKLIRNQRFPASYHHAAETVVNMLM	PHITQKFGDNPEA---SKNANHS LAV	956
hCLASP7	ALHLLLGQRDLTERKLRFPGRFLDDITALVGS	VGLEVITRVHKDEL---AEHLNASLAF	999
hCLASP1	AQHLIDTNKIQLHRPQRFEPESYQNELDNLVM	VLSDHVIWKYKDALEE---TRRATHSVAR	1052
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hCLASP4	FLKRCCLTMDRGFIENLINDYISGFSPKDP	-----KVLAEYKFEFLQTICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVFNIRHYCSQLSAKLSNL	---HTLISMRLEFLRILCSHEHYLN	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSL	PNPSVLVSLRLDFLRIICSHEHYVT	1136
hCLASP2	FIKRCFTFMDRGFVFKQINNYISCFAPGDP	-----KTLFEYKFEFLRVVCNHEHYI	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSS	PNPAALLTLRMEFTRILCSHEHYVT	1059
hCLASP1	FLKRCFTFMDRGCVFEMVNNYISMFS	SGDL-----KTLQYKFDLQEVQCHEFI	1107
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Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGLLRETSI 1060
hCLASP5 FFMNADTAPTSP--CPSISSQNSSSSCSFQDKIASMFDLTSEYRQOHFLTGLFTLAA 1085
hCLASP3 PCSLLTPPASPSVSSATSQSSGFSTNVQDKIANMFELSVFPQOQHYLAGI VLTELAV 1196
hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFNRHFLVGLLREVT 1052
hCLASP7 PCCPLSPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQOQHYLAGI LTELAL 1119
hCLASP1 PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGILLREVG 1157

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hCLASP4 ALQDN---YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQLYLPFVGLLENIRL 1116
hCLASP5 ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAALYLPVGIILDALP-- 1143
hCLASP3 ILDPDAEGLFGLHKKVINMVHLLSSHSDPRYSDPQIKARVAMLYLPLIGIMETVP-- 1254
hCLASP2 ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVORI 1108
hCLASP7 ALEPEAEGAFLLHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP-- 1177
hCLASP1 ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPLYGMLLDNMPRI 1213

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hCLASP4 AGRDTLYSCA-----AMPN-S---ASRDEFFPCGFTSPANRGSLSLTDKDTAYGS 1160
hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162
hCLASP3 -----QLY-----DFTETHNQGRPICIAATDD-- 1276
hCLASP2 NVRDVSPFPVNAGMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167
hCLASP7 -----RLH-----DFAEGPGQRSRLASMLDSDTE 1201
hCLASP1 YLKDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFSDVLNSIAAFSSIAIS 1273

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hCLASP4 FQ-NGHGIKREDSRGLIPEGATGFDPQNGTGEN-----TRQSSSTRSSVSQYNRLDQYE 1213
hCLASP5 -----EEQEGAGAINQNALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT 1208
hCLASP3 -----YESEGSMISQTVAMAIAGTSVPQLTR---PGSFLLTSTSGRQHTTFSAES 1324
hCLASP2 STPNINSVRNADSRGLISTDSGNSLPERNSEKNSLDKHQQSSTLGNSVVRCDKLDQSE 1227
hCLASP7 -----GEGDIAGTINPSVAMAIAGGFLAPGSR---ASISQGPPTASRAGCALSAES 1249
hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327

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hCLASP4 TRSLLMCYLYIVKMISEDTLTYWNKVSPOELINILILEVCLFHFRYMGRNIARVHDA 1273
hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLDFICVLCFEYKKGQSSDKVSTQ 1268
hCLASP3 SRSLLICLLWVLKNADETVLQKWFTDLSVLQNLRLDLLYLVCVSCFEYKKGKVFERNLSL 1384
hCLASP2 IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFYMGKRYIARNQEG 1287
hCLASP7 SRTLLACVLWVLKNTPEALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKKGKKAFERINSL 1309
hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQRAPSPESVDFFSILDVCLQNFYRLGKRNIIIRKIAA 1387

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hCLASP4 WLSKHFGIDR-----KSQTMPALRNRSQVMQARLQHLSSLESS----- 1311
hCLASP5 VLQKSRDVKAR-----LEEALLRGEARGEMMRRRAPGNDRFPGLNEN-- 1311
hCLASP3 TFKKSKDMRAK-----LEEAILGSI GARQEMVRRSRGQLERSPSGSAGFSQ 1430
hCLASP2 LGPIVHDRKS-----QTLPVSRNRTGMHARLQQLGSLDNS----- 1323
hCLASP7 TFKKSLDMKAR-----LEEAILGTIGARQEMVRRSRERSPFGNPEN----- 1350
hCLASP1 AFKFVQSTQNNGTILKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----- 1442

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hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQCFTQLL 1359
hCLASP5 --LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD 1368
hCLASP3 ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVVQTVS-VTE 1489
hCLASP2 -----LTFNHSYGHSDADVHLHQSLLLEANIATEVCLTALDTLSLFTLAFKNQLL 1371
hCLASP7 --VRWRKSVTHWKQTSRVDKTKDEMEHEALVEGNLATEASLVVLDLLEIIVQTVM-LSE 1407
hCLASP1 --ALSNPKLLQMLDNTMTSNEIDIVHHVDTEANIATEGCLTILDVLSLFTQTHORQLQ 1500

hCLASP4 NNDGHNPLMKKVFVDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFCY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCQSTTYLTHCFATLRALIAKFGDLLFEEVEQCFLCH 1425
hCLASP3 SKES---ILGGVLKVLHSHMACNQSAVYLQHCFAQRALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPMLMKKVFVDVYLCFLQKHQSETALKNVFTALRSIYKFPSTFYEGADMCAALCY 1431
hCLASP7 ARE---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCAIDLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLVCKFPSAFFQGPADLCGSFCY 1560
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hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIVSSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMVDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVTMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIIISVSQIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSSQLIADAG-IGG 1619
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hCLASP4 SRFQESLFIINNANSRPMKATAFPAEVKDLTKRIRTVLMATAQMKHEKDPEMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFFPTQVEELLCLNLSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTLTYAEDLELRETTFFDQVQDLVFNLMILSDTVKMKHEQEDPEMLIDLQ 1664
hCLASP2 TRFQQSLSIINNANSRDLIKHTSFSSDVKDLTKRIRTVLMATAQMKHEKDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTLTYAEDMGLRDSFPAEQVQDLVFNLMILSDTVKMKHEQEDPEMLIDLQ 1582
hCLASP1 SRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLMATAQMKHEKDPEMLVDLQ 1679
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transmembrane
hCLASP4 YSLAKSYASTPELRKTWLDMAKIHVKNGD FSEAAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRLTWLQNMMAEKHTKKKCYTEAAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEAAQCLVHSAALVAEYLSMLEDH----- 1718
hCLASP2 YSLAKSYASTPELRKTWLDMAKIHVKNGD LSEAAMCYVHVTALVAEYLTRKG----- 1604
hCLASP7 YRIARGYQGPSDLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYLALLEDDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGD LSEAAMCYIHIAALIAEYLKRKGWYKVEKI 1739
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-----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD---- 1622
-----SYLPVGSVSFQNISSNVLEESVVSSEDTLSPDEEDGV 1633
-----KYLPGCVTFQNISSNVLEESAVSDDVVSPEDEGI 1753
-----VFRQGCTAFRVITPNIDEESMMEDVGMQD----- 1634
-----RHLPGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
CTASLLSEDTHPCDNSLLTTPSGGSMFSGWPAFLSITPNIKEEGAAKEDSGMHD---- 1795
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ITAM
hCLASP4 ---VHYSEEVILLELLEQCVDGLWKAERYEIISEISKLVPIYKRRFEKLTQVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKLVIPILEANRDAKKLSTIHGKLQE 1813
hCLASP2 ---VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIYKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLAAVHGKLQE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSEYELIADVKNPIIAVFEKQDFKLSLDLYDTHR 1852
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ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKILEVMHTKKRLGLTFFRVAFYQSFEEEDGKEYIYKEKLTGLSEISLRLVKIYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQEYVYKEHAITKLPEISHRLEAFYG 1750
hCLASP3 AFSKIYHQSTGWERMFGTYFRVGFFG-TKFGDLDEQEYVYKEHAITKLAEISHRLEAFYG 1872
hCLASP2 -----LFFEDGKEYIYKEKLTPLSEISQRLKLYG 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFFG-AHFGDLDEQEYVYKEHSITKLAEISHRLEAFYT 1791
-----LFFEDGKEYIYKEKLTGLSEISQRLKLYG 1710

	ITAM	ITAM	
hCLASP4	ERFGTENVKIIQSDSKVNAKELDPHYAHIQVITYVKEYFDDKELTERKTEFERNHNISRFV		1799
hCLASP5	QCFGAEFVEVIKDSIPVDKTKLDPNKAYIQITFVEEYFDEYEMKDRVITYFEKNFNLRFRM		1810
hCLASP3	ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITFVEEYFDYEMKDRITYFDKNYNLRFRM		1932
hCLASP2	DKFGSENVKMIQDSGKVNPKDLDSHYAYIQVTHVIEFFDEKELQERKTEFERSHNIRFRM		1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSCKAYIQITFVEEYFDYELKDRVITYFDRNYGLRTFL		1851
hCLASP1	DKFGADNVKIIQDSNKVNPKDLDPHYAYIQVITYVTEFFEEKEIEDRKTDFFEMHHNINRFV		1972
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	ITAM	DOCK motif	
hCLASP4	FEAPYTLGKKGQGCIEEQKRRRTILTTSNSFFVVKRIPINCEQQINLKPIDGATDEIKD		1859
hCLASP5	YTFPFTLEGRPRGELHEQYRRNTVLTTMHAFYIKTRISVIQKEEFVLTPIEVAIEDMKK		1870
hCLASP3	YCTPFTLDGRAHGEHEQFKRKTILTTSHAFYIKTRVNVTHKEEILTPIEVAIEDMQK		1992
hCLASP2	FEMPFTQTGKROGGVEEQKRRRTILTAHCFYVVKRIPVMYQHHTDLNPIEVAIDEMSK		1830
hCLASP7	FCTPFTPDGRAHGEPEQHKRKTLLSTDHAFYIKTRIRVCHREETVLTPIEVAIEDMQK		1911
hCLASP1	FETPFTLSGKKHGGVAEQKRRRTILTSHLFFVVKRIQVISQSSTELNPIEVAIDEMSR		2032
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	Coiled-coil	
hCLASP4	KTAELQKLCSSTDVDMIQQLKLQGVWSVQVNAGPLAYARAFNLDSQASKYPPKKVSELK	1919
hCLASP5	KTLQLAVAINQEPDAKMLQMLVQGSVGATVNOGPLEVAQVFLAEIPADPKLYRHHNKLK	1930
hCLASP3	KTQELAFATHQDPADPKMLQMLVQGSVGTTVNOGPLEVAQVFLSEIPSDPKLFRHHNKLK	2052
hCLASP2	KVAELRQLCSSAEVDMIKLQKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLK	1890
hCLASP7	KTRELAFATEQDPPDAKMLQMLVQGSVGPTVNOGPLEVAQVFLAEIPEDPKLFRHHNKLK	1971
hCLASP1	KVSELNQLCTMEEVDMISLQKLQGSVSVKNAGPMAYARAFLEETNAKKYPDNQVKLLK	2092
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	Coiled-coil	
hCLASP4	DMFRKFIQACSIAELNERLIKEDQVEYHEGLKSNFRDMVKELSDIIHEQILQEDTMHSP	1979
hCLASP5	LCFKFIMRCGRGAVEKNKRLITADQREYQQLKKNYNKLKENLRPMIERKIPELYKPIFR	1990
hCLASP3	LCFKDFTKRCEDALRKNKSLIGPVQKEYQRELGLKSSP-----	2090
hCLASP2	EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEKTS-	1949
hCLASP7	LCFKDFCKKCEDALRKNKALIGPDQKEYHRELERNYCRLREALQPIILTQRLPQLMAPTP-	2030
hCLASP1	EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKDMSELSTVMNEQITGRDDLKSR	2152
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	PDZ ligand	
hCLASP4	WMSNTLHVFCASISGTSSDRGYGSPHYAEV--	2008
hCLASP5	VESQKRDSFHRSSFRCETQLSQGS-----	2015
hCLASP3	-----	
hCLASP2	VLPNSLHIFNAISGTPTSTMVHGMTSSSSVV	1980
hCLASP7	--PGLRNSLNRSFRKADL-----	2047
hCLASP1	GVDQCTRVISKATPALPTVSISSSAEV--	2180